Dygunes Ceryol

(A) FBD(1,2) fused at t	SK		1	2	<u> </u>
(B) FBD(4,5) fused at t	he Caterminal of SK				:
(B) FBD(4,3) lused at v	SK		4	5	_
Ĺ					
(C) FBD(4,5) fused at 1	the N-terminal of SK	<u> </u>			
4 5	SK				
(D) EDD(4.5) fused at 1	ooth the C as well as N-ter	minals of SK	:		·.
(D) FBD(4,3) Iuseu at 1	SK		4	5	

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DOGHOESS CAEFOL

Fig. 2

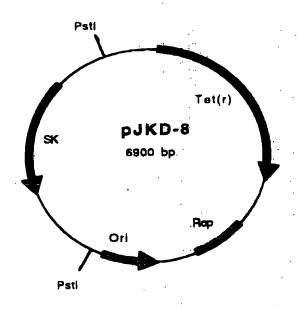


Fig. 3

31/11 ATT GCT GGA CCT GAG TOG CTG CTA GAC CCT CCA TCT GTC AAC AGC CAA TTA GTT GTT 1/1 ile ala giy pro giu trp: leu leu asp arg pro ser val asn asn ser gln leu val val 91/31 61/21NGC GTT GCT GGT ACT GTT GAG GGG ACG AAT CAA GAC ATT AGT CIT AAA TTT TIT GAA ATC ser val ala gly thr val glu gly thr asm glm asp ile ser leu lys phe phe glu ile 151/51 121/41 GAT CTA ACA TOA CGA CCT GCT CAT GGA GGA AAG ACA GAG CAA GGC TTA AGT CCA AAA TCA asp leu the ser arg pro ala his gly gly lys the glu gln gly leu ser pro lys ser 211/71 181/61 AAA CCA TIT GCT ACT GAT AGT GGC GCG ATG TCA CAT AAA CIT GAG AAA GCT GAC TTA CTA lys pro phe ala thr asp ser gly ala met ser his lys leu glu lys ala asp leu leu 271/91 241/81 AAG GCT ATT CAA GAA CAA TIG ATC GCT AAC GTC CAC AGT AAC GAC GAC TAC TIT GAG GTC lys ala ile gin glu gin leu ile ala asn val his ser asn asp asp tyr phe glu val 331/111 301/101 ATT GAT TIT GCA AGC GAT GCA ACC ATT ACT GAT CGA AAC GGC AAG GTC TAC TIT GCT GAC ile asp phe ala ser asp ala thr ile thr asp arg ash gly lys val tyr phe ala asp 391/131 AAA GAT GGT TOG GTA ACC TTG CCG ACC CAA CCT GTC CAA GAA TTT TTG CTA AGC GGA CAT 361/121 lys asp gly ser val the leu pro the gln pro val gln glu phe leu leu ser gly his 451/151 421/141 GTG COC GTT AGA CCA TAT AAA GAA AAA CCA ATA CAA AAC CAA GCG AAA TCT GTT GAT GTG val arg val arg pro tyr lys glu lys pro ile gln asn gln ala lys ser val asp val 511/171 481/161 GAR TAT ACT GTA CAG TIT ACT CCC TTA AAC CCT GAT GAC GAT TTC AGA CCA GGT CTC AAA glu tyr thr wal gin phe thr pro leu asn pro asp asp phe arg pro gly leu lys 571/191 541/181 GAT ACT AAG CTA TIG AAA ACA CTA GCT ATC GGT GAC ACC ATC ACA TCT CAA GAA TTA CTA asp thr lys leu leu lys thr leu ala ile gly asp thr ile thr ser gln glu leu leu 631/211 CCT CAA GCA CAA AGC ATT TTA AAC AAA AAC CAC CCA GGC TAT ACG ATT TAT GAA CGT GAC 601/201. ala gin ala gin ser ile leu asn lys asn his pro gly tyr thr ile tyr glu arg asp 691/231 TOO TEA ATC GIT ACT CAT GAC AAT GAC ATT TTC CGT ACG ATT TTA CCA ATG GAT CAA GAG 661/221 ser ser ile val thu his asp asn asp ile phe arg thr ile leu pro met asp gln glu 751/251 TIT ACT TAC COT GIT AMA MAT COG GAM CAM GCT TAT AGG ATC MAT AMA MAM TOT GGT CTG 721/241 phe thr tyr arg val lys asn arg glu gln ala tyr arg ile asn lys lys ser gly leu 811/271 MAT CAN GAR ATA AND ARC ACT GAC CTG ATC TCT GAG ARA TAT TAC GTC CIT ARA ARA GGG 781/261 ash gin glu ile ash ash thr asp leu ile ser glu lys tyr tyr val leu lys lys gly 871/291 GAA AAG COG TAT GAT COC: TIT GAT COC AGT CAC TIT AAA CIG TITC ACC AIC AAA TAC GIT 841/281 glu lys pro tyr amp pro phe asp arg ser his leu lys leu phe thr ile lys tyr val 931/311 901/301 CAT CIT GAT ACC AAC GAA TTC CTA AAA AGT GAG CAG CIT TTA ACA GCT AGC GAA CGT AAC asp val asp thr ash glu leu leu lys sor glu gln leu leu thr ala ser glu arg ash 991/331 TTA CAC TTC ACA CAT TTA TAC GAT CCT CGT CAT AAG GCT AAA CTA CTC TAC AAC AAT CTC lou asp phe arg asp leu tyr asp pro arg asp lys ala lys leu leu tyr asn asn leu 1051/351 1021/341 CAT GCT TIT GGT ATT ATG GAC TAT ACC TTA ACT GGA AAA GTA GAG GAT AAT CAC GAT GAC asp ala phe gly ile met asp tyr thr leu thr gly lys val glu asp asn his asp asp 1111/371 ACC AAC COT ATC ATA ACC OTT TAT ATG GOC AAG COA CCC GAA GGA GAG AAT GCT AGC TAT thr asn arg ile ile thr val tyr met gly lys arg pro glu gly glu asn ala ser tyr 1171/391 CAT THA GCC TAT CAT ARA GAT CGT TAT ACC GAR GAR GAR CAR GAR GTT TAC ACC TAC CTG his leu ala tyr asp lys asp arg tyr thr glu glu glu arg glu val tyr ser tyr leu 1231/411 COT TAT ACA GOG ACA COT ATA COT GAT AAC COT AAC GAC AAA TAA arg tyr thr gly the pro the pro asp asn pro asn asp lys OCH

```
694 Spil
676 Msil
                                                 533 BsmAl
                                                 532 Eco31 |
                                                528 SexAl
                                                              675 BspH1
                                      417 Nsp i
                                                            660 BaeR I
                                      417 BspLU111
                                 417 AII III
372 Bate II
                                                            658 Ple I
                                                          633 Sec I
                                                                                 876 Xmn I
                                                        618 Ahalll
                                                                                                         1128 Bsm I
1128 Bsm I
1153 BsaB I
                                    408 Esp I
                       258 Mfe I
  37 Hind II
                                                                                            986 Bal I
                                                                            818 Ssp I
                                                527 Tth1111
              165 All II
                               346 Acc |
7 'Ava II-
                                                                                          966 Eco57 I
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                                             489 Bsp1407 I
           138 BsiY I
                          310 Mwo I
7 Asu l
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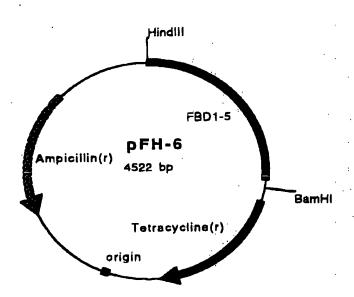
1245 base pairs

Unique Sites

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SK.DNA

Fig. 5



1994DEZE DAEZOX

Fig. 6

31/11. CAG GCT CAG CAA ATG GTT CAG CCC CAG TCC CCG GTG GCT GTC ACT CAA AGC AAG CCC CGT gin ala gin gin met val gin pro gin ser pro val ala val ser gin ser lys pro gly 91/31 TOT THE GAC ANT GGA ANA CAC THE CAG ATA ANT CAN CAG TOG GAG COG ACC THE CITA GGT cys tyr asp asn gly lys his tyr gln ile asn gln gln trp glu arg thr tyr leu gly 151/51 121/41 AAT GIG TIG GIT TGT ACT TGT TAT GGA GGA AGC CGA GGT TIT AAC TGC GAA AGT AAA CCT ash val leu wal cys thr cys tyr gly gly ser arg gly phe ash cys glu ser lys pro 211/71 GAA GOT GAA GAG ACT TOO TIT GAC AAG TAC ACT GOG AAC ACT TAC CGA GTG GGT GAC ACT glu ala glu glu thr cys phe asp lys tyr thr gly asn thr tyr arg val gly asp thr 271/91 TAT GAG COT CCT AAA GAC TCC ATG ATC TOO GAC TOT ACC TGC ATC GGG GCT GGG CGA GCG 241/81 tyr glu arg pro lys asp ser met ile trp asp cys thr cys ile gly ala gly arg gly 331/111 AGA ATA AGC TOT ACC ATC GCA AAC CGC TGC CAT GAA GGG GCT CAG TCC TAC AAG ATT GGT 301/101 arg ile ser cys thr ile ala asn arg cys his glu gly gly gln ser tyr lys ile gly 391/131 361/121 CAC ACC TOG ACG ACA CCA CAT GAG ACT GGT GGT TAC ATG TTA GAG TGT GTG TGT CTT GGT asp thr trp arg arg pro his glu thr gly gly tyr met leu glu cys val cys leu gly 451/151 421/141 AAT GCA AAA GCA GAA TOG ACC TGC AAG CCC ATA GCT CAG AAG TGT TIT GAT CAT GCT GCT asn gly lys gly glu trp thr cys lys pro ile ala glu lys cys phe asp his ala ala 511/171 481/161 OCC ACT TOO TAT GIG GIC GGA GAA ACG TOG GAG AAG CCC TAC CAA GGC TOG ATG ATG GIA gly the ser tyr val val gly glu the trp glu lys pro tyr gln gly trp met met val 571/191 541/181 CAT TOT ACT TOO CTG GGA GAA GGC AGC GGA CGC ATC ACT TGC ACT TOT AGA AAT AGA TOO asp cys thr cys leu gly glu gly ser gly arg ile thr cys thr ser arg ash arg cys 631/211 601/201 and gat cag gad aca agg aca too tat aga att gga gad acc tog agg ang ang gat aat asn asp gin asp thr arg thr ser tyr arg ile gly asp thr trp ser lys lys asp asn 691/231 661/221 CGA GGA AAC CTG CTC CAG TGC ATC TGC ACA GGC AAC GGC CCA GGA GAG TGG AAG TGT GAG arg gly asn leu leu gln cys ile cys thr gly asn gly arg gly glu trp lys cys glu 751/251 721/241 AGG CAC AGG TOT GTG CAG AGG AGA TOG AGG GGA TOT GGG CCC TTC AGG GAT GTT CGT arg his thr ser wal glm thr thr ser ser gly ser gly pro phe thr asp wal arg

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Fig. 7

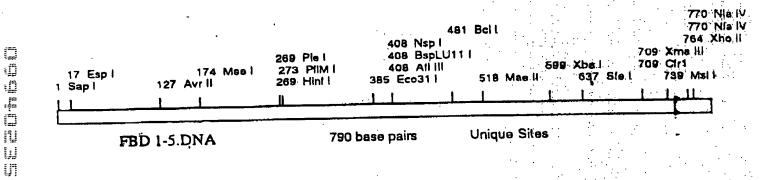


Fig. 8

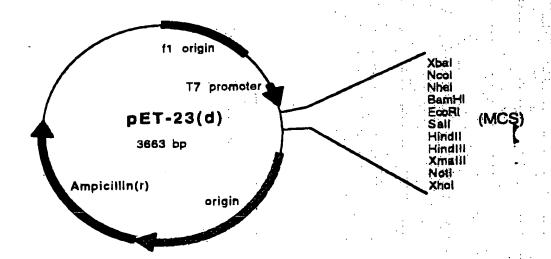
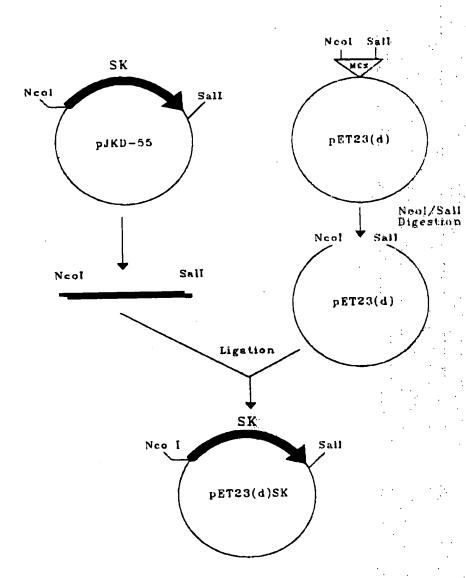
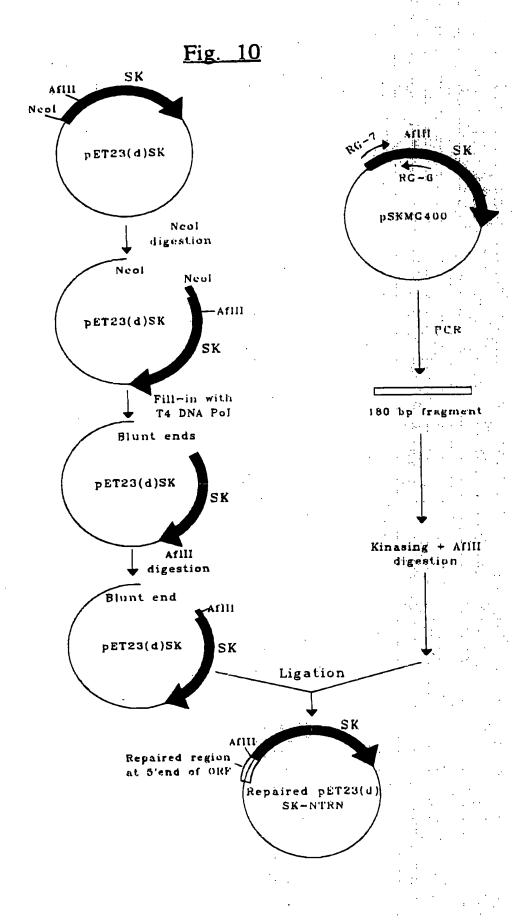


Fig. 9



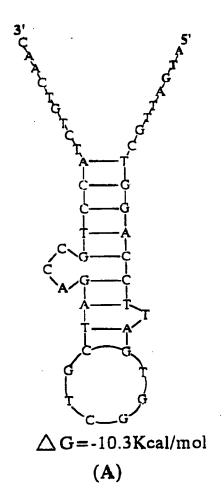
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DGG4UES GEE701

Fig. 11

	10	20	- 30	4,0::	50
	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
51	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
101		GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
151	CTGCTAGACC	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TITTTTGAAA
201	TGGTACTGTT	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
251	TCGATCTAAC AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TOTCACATAA
301		GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
351	ACTTGAGAAA ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
401		CTGATCGAAA	CGGCAAGGTC	TACTITGCTG	ACAAAGATGG
451	GCAACCATTA TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTTG	CTAAGCGGAC
501	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
551	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
601	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
651	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
701	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTOCTOAAT
751	CGTCACTCAT	GACAATGACA	TITICCGTAC	GATTTTACCA :	ATGGATCAAG
801	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	
851	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
901	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
951	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1001	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1051	CAGAGATITA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1101	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1151	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1201			ATCATTTAGC	CTATGATAAA	GATCGTTATA
1251	CGAAGGAGAG CCGAAGAAGA		TACAGCTACC	TGCGTTATAC	AGGGACACCT
1301		ACCCTAACGA	CAAATAA	. •	
1351	ATACCTGATA	ACCEIANCON	4 .		



 $\triangle G = -5.0$ Kcal/mol (B)

Fig. 13

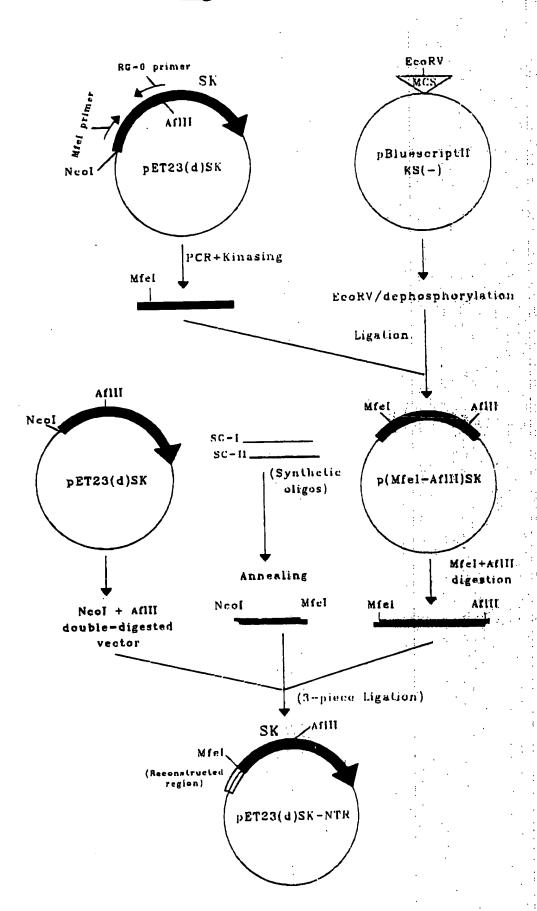
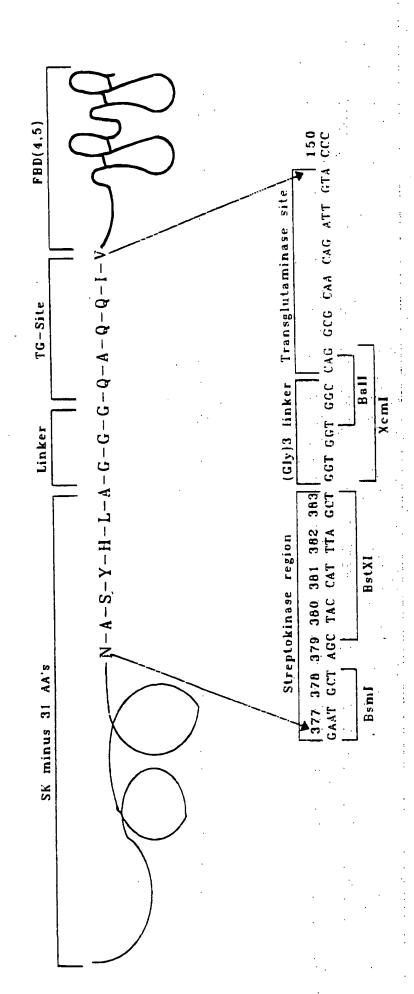


Fig. 14

	10	20	30	40	50
	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
51	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATAGCTGG.	TCCTGAATGG
101	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGEGTTGC
151	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
201	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
251	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TOTCACATAA
301	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
351	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
401	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
451	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATITTTG	CTAAGCGGAC
501	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
551	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
601	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
651	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
701	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TAT GAACGTG	ACTCCTCAAT
751	CGTCACTCAT	GACAATGACA	TTT TCCGTAC	GATTTTACCA	ATGGATCAAG
801	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
851	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
901	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
951	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1001	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1051	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1101	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1151	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1201	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CTATGATAAA	GATCGTTATA
1251	CCGAAGAAGA	ACGAGAAGTT	TACAGCTACC	TGCGTTATAC	AGGGACACCT
1301	ATACCTGATA	ACCCTAACGA	CAAATAA	•	

Fig. 15



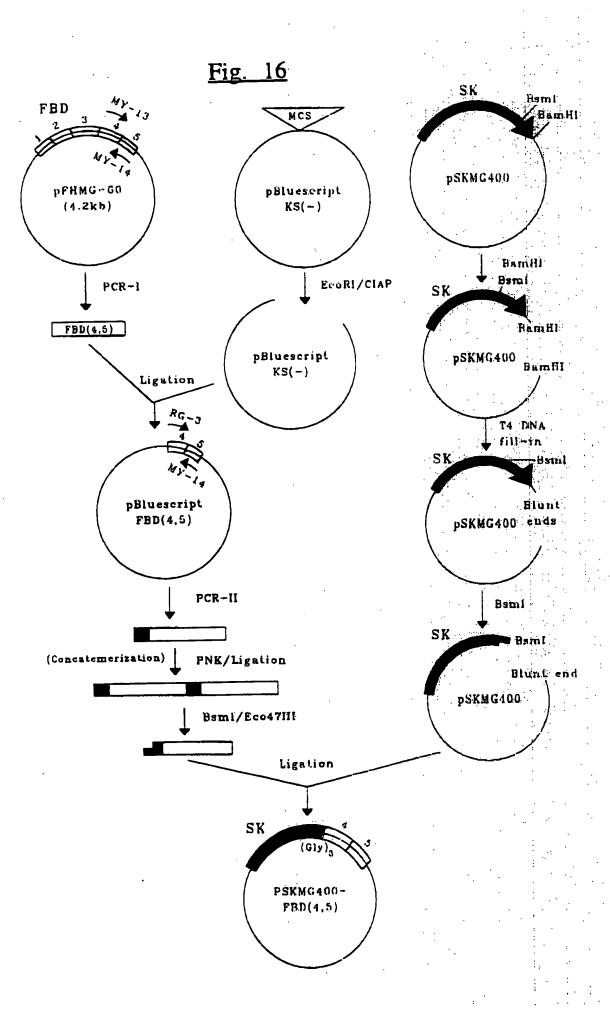
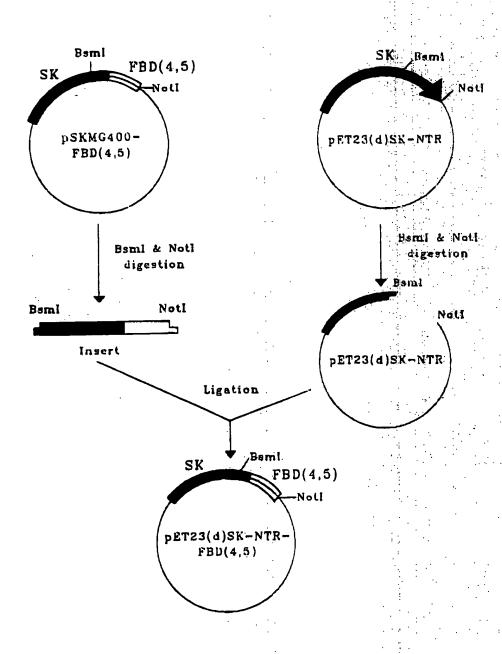


Fig. 17a



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	10	20	30	40	50
	TITGTTTAAC	TITAAGAAGG	AGATATACCA	TGATAGCTGG	TCCTGAATGG
51 .	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGCGTTGC
101	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
151	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
201	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
251	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
301	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATIT	TGCAAGCGAT
351	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
401	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTTG	CTAAGCGGAC
451	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
501	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
551	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA.	ACACTAGCTA
601	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
651	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TAT GAACGTG	ACTCCTCAAT
701	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
751	AGTITACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
801	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
85]	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
901	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
. 951	TTGCTAAAAA	GTGAGCAGCT	CITAACAGCT	AGCGAACGTA	ACTTAGACTT
1001	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAA ACTACTC	TACAACAATC
1051	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1101	AATCACGATG	ACACCAACCG	TAT CATAACC	GTTTATATGG	GCAAGCGACC
1151	CGAAGGAGAG	AATGCTAGCT	ACCATTTAGC	TGGTGGTGGC	
1201	AGATTGTACC	CATAGCTGAG	AAGTGTTTTG	ATCATGCTGC	TGGGACTTCC
1251	TATGTGGTCG	GAGAAACGTG	GGAGAAGCCC	TACCAAGGCT	GGATGATGGT
1301	AGATTGTACT	TGCCTGGGAG	AAGGCAGCGG	ACGCATCACT	TGCACTTCTA
1351	GAAATAGATG	CAACGATCAG	GACACAAGGA	CATCCTATAG	AATTGGAGAC
1401	ACCTGGAGCA	AGAAGGATAA	TCGAGGAAAC	CTGCTCCAGT	GCATCTGCAC
1451	AGGCAACGGC	CGAGGAGAGT	GGAAGTGTGA	GAGGCACACC	TCTGTGCAGA
1501	CCACATCGAG	CGGATCTGGC	CCCTTCACCG	ATGTTCGTTA	G
			and the second s		

Fig. 18

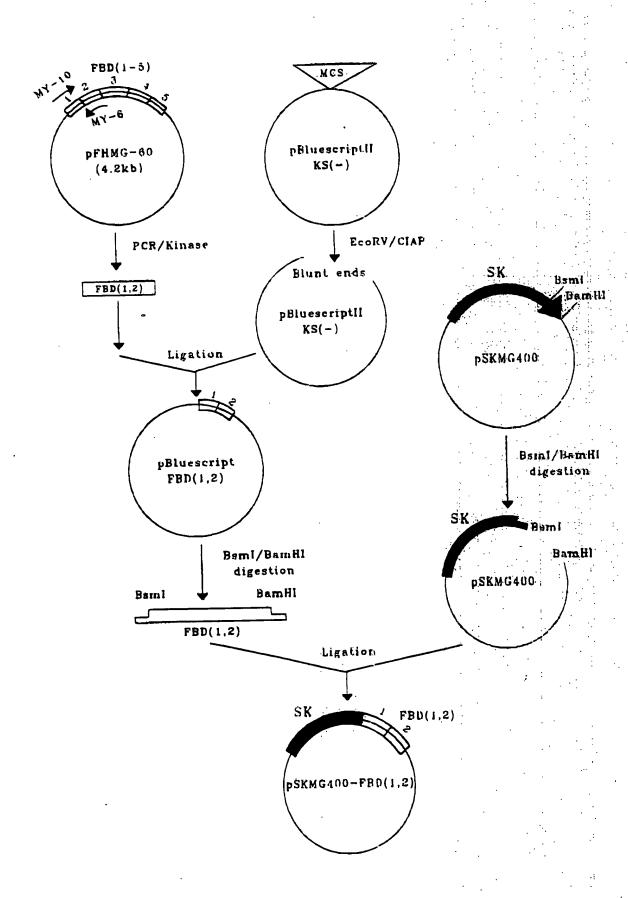
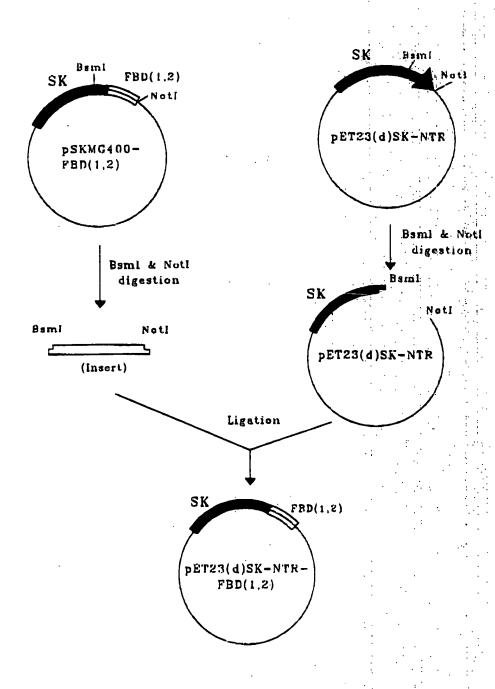


Fig. 19a



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	10	20	30	40	50
	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
51	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
101	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
151	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
201	CTGCTAGACC	GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
251	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
301	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
351	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA.	TGTCACATAA
401	ACTTGAGAAA	GCTGACITAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
451	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
501	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
551	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATITITG	CTAAGCGGAC
601	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
651	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACICCCITAA	ACCCTGATGA
701	CGATTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
751	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
801	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
851	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
901	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
951	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
1001	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1051	GTCACTTGAA	ACTGTTCACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1101	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA.	ACTTAGACTT
1151	CAGAGATITA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1201	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1251 -	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1301	CGAAGGAGAG	AATGCTAGCT	ATCATITAGC	CGGTGGTGGT	CAGGCGCAGC
1351	AAATGGTTCA	GCCCCAGTCC	CCGGTGGCTG	TCAGTCAAAG	CAAGCCCGGT
1401	TGTTATGACA	ATGGAAAACA	CTATCAGATA	AATCAACAGT	GGGAGCGGAC
1451	CTACCTAGGT	AATGTGTTGG	TTTGTACTTG	TTATGGAGGA	AGCCGAGGTT
1501	TTAACTGCGA	AAGTAAACCT	GAAGCTGAAG	AGACTTGCTT	TGACAAGTAC
1551	ACTGGGAACA	CTTACCGAGT	GGGTGACACT	TATGAGCGTC	CTAAAGACTC
1601	CATGATCTGG	GACTGTACCT	GCATCGGGGC	TGGGCGAGGG	AGAATAAGCT
1651	GTACCATCTA	A		•	

Fig. 20

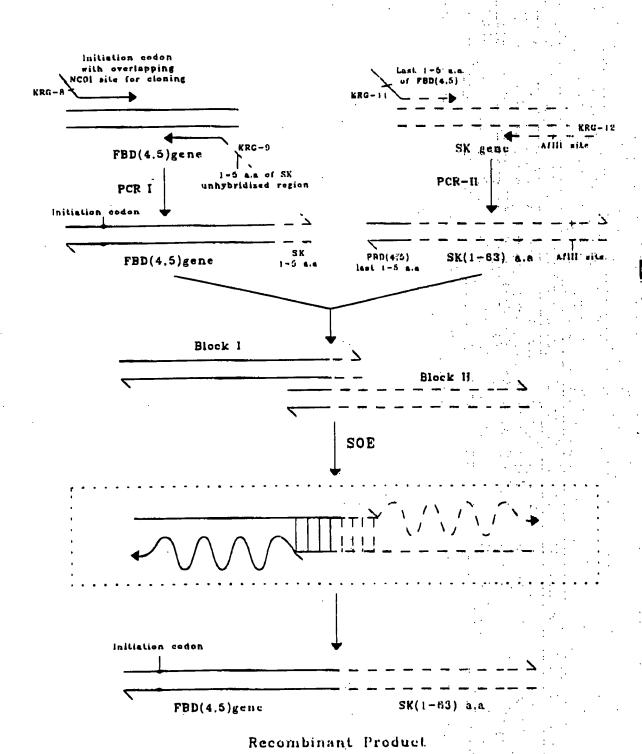


Fig. 21a

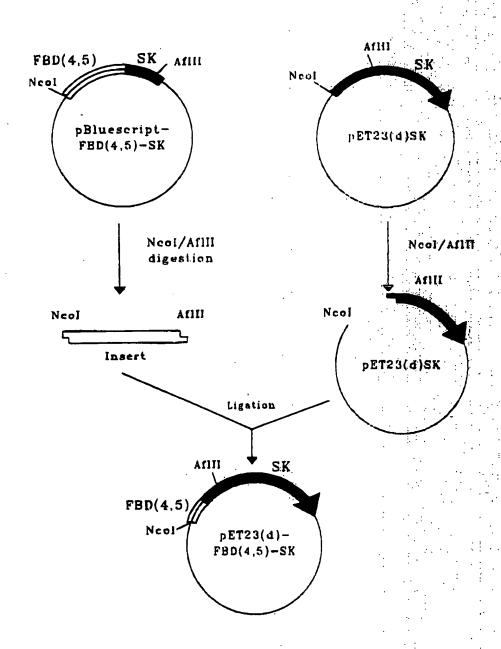
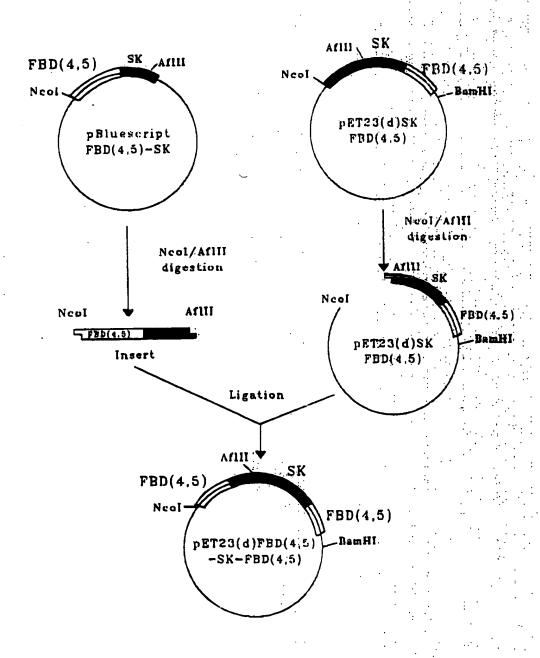


Fig. 21b

	10	20	30	40	50
1	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT	AACCAGTAAG
51	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
101	GCACCCGTGG	CCAGGACCCA	ACCCTGCCCG	AGATCTCGAT	CCCGCGAAAT
151	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
201	TTTGTTTAAC	TTTAAGAAGG	AGATATACEA	TGGTGCAAGC	ACAACAGATT
251	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
301	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACTTCTAG
351	AAATAGATGC	AACGATCAGG	ACACAAGG AC	ATCCTATAGA	ATTGGAGACA
401	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
451	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCACACCT	CTGTGCAGAC
501	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTCGTATT	GCTGGACCTG
551	AGTGGCTGCT	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GGTTGTTAGC
601	GTTGCTGGTA	CTGTTGAGGG	GACGAATCAA	GACATTAGTC	TTAAATTTT
651	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG	ACAGAGCAAG
701	GCTTAAGTCC	AAAATCAAAA	CCATTTGCTA	CTGATAGTGG	CGCGATGTCA
751	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG	AACAATTGAT
801	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTTTGCAA
851	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
901	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	GTCCAAGAAT	TTTTGCTAAG
951	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA	CAAAACCAAG
1001	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGITTACTCC	CTTAAACCCT
1051	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT	TGAAAACACT
1101	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGCT	CAAGCACAAA
1151	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
. 1201	TCAATCGTCA	CTCATGACAA	TGACATTITC	CGTACGATTT	TACCAATGGA
1251	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT	TATAGGATCA
1301	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1351	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA
1401	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTCGATACCA
1451	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACTTA
1501	GACTTCAGAG	ATTTATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1551	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	GGAAAAGTAG
1601	AGGATAATCA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATOGGCAAG
1651	CGACCCGAAG	GAGAGAATGC	TAGCTATCAT	TTAGCCTATG	ATAAAGATCO
1701	TTATACCGAA	GAAGAACGAG	AAGTTTACAG	CTACCTGCGT	TATACAGGGA
1751	CACCTATACC	TGATAACCCT	AACGACAAAT	AA	· .

Fig. 22a

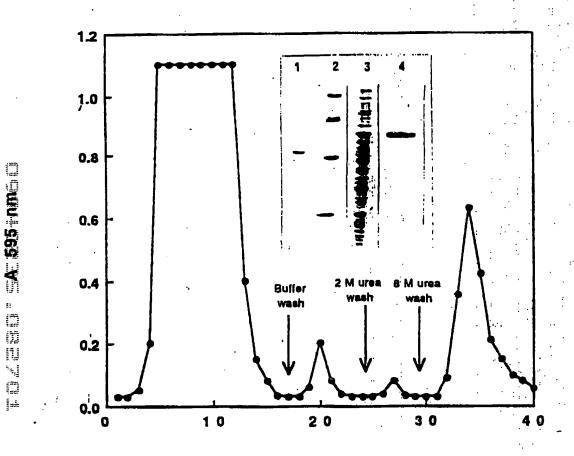


ב-חבר-דששם דם. של בגחון גרוועעני מי בנים

Fig. 22b

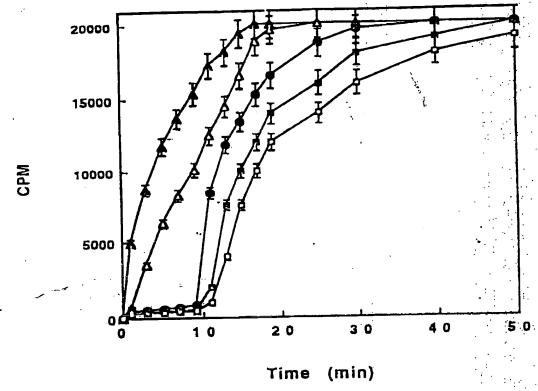
	10	20	30	40	50
1	CGAAGACCAT	TCATGTTGTT	GCTCAGGTCG	CAGACGTTTT	GCAGCAGCAG
51	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT -	AACCAGTAAG
101	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
151	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
201	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC ::	TAGAAATAAT
251	TITGTTTAAC	TTTAAGAAGG	AGATATACCA	'IGGTGCAAGC	ACAACAGATT
301	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
351	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACTTCTAG
401	AAATAGATGC	AACGATCAGG	ACACAAGGAC	ATCCTATAGA	ATTGGAGAGA
451	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
501	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCAÇĂÇĈT	CTGTGCAGAC
551	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTCGTATT	GCTGGACCTG
601	AGTGGCTGCT-	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GCTTCTTAGC
651	GTTGCTGGTA	CTGTTGAGGG	GACGAATCAA	GACATTAGTC	TTAAATTTTT
701	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG	ACAGAGCAAG
751	GCTTAAGTCC	AAAATCAAAA	CCATTTGCTA	CTGATAGTGG:	CCCGATGTCA
801	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG	AACAATTGAT
851	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTTTGCAA
901	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
951	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	CTCCAAGAAT	TTTTGCTAAG
1001	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA	CAAAACCAAG
1051	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGTITACTCC	CTTAAACCCT
1101	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT	TGAAAACACT
1151	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGCT	CAAGCACAAA
1201	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
1251	TCAATCGTCA	CTCATGAÇAA	TGACATTTTC	CGTACGATIT	TACCAATGGA
1301	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT.	TATAGGATCA
1351	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1401	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA
1451	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTCGATACCA
1501	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACTTA
1551	GACTTCAGAG	ATTTATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1601	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	
1651	AGGATAATCA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATGGGCAAG
1701	CGACCCGAAG	GAGAGAATGC	TAGCTACCAT	TTAGCTGGTG	GTGGCCAGGC
1751	GCAACAGATT	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA
1801	CTTCCTATGT	GGTCGGAGAA	ACGTGGGAGA	AGCCCTACCA	AGGCTGGATG
1851	ATGGTAGATT	GTACTTGCCT	GGGAGAAGGC	AGCGGACGCA	TCACTTGCAC
1901	TTCTAGAAAT	AGATGCAACG	ATCAGGACAC	AAGGACATCC.	TATAGAATTG
1951	GAGACACCTG	GAGCAAGAAG	GATAATCGAG	GAAACCTGCT	CCAGTGCATC
2001	TGCACAGGCA	ACGGCCGAGG	AGAGTGGAAG	TGTGAGAGGC	ACACCTCIGT
2051	GCAGACCACA	TCGAGCGGAT	CTGGCCCCTT	CACCGATGTT	CCTTAG

Fig. 23



Fraction No.

Fig. 24



<u>nggunama loguyut</u>